RAW SEQUENCE LISTING ERROR REPORT
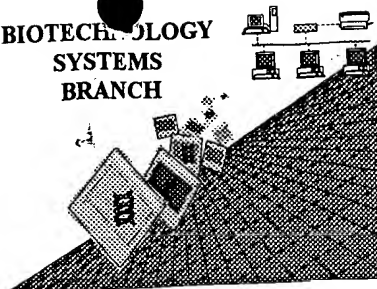
BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/852,058

Source: OIPE

Date Processed by STIC: 10/10/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/852,058 |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics / Wrapped Aminos
: The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length
: The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering
: The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII
: The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length
: Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug"
: A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES)
: Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES)
: Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES)
: Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response
: Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>
: Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug"
: Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n
: n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/852,058

DATE: 10/10/2001
TIME: 17:07:04

Input Set : A:\2404640.diatech.method.ST25.txt
Output Set: N:\CRF3\10102001\I852058.raw

```
 3 <110> APPLICANT: Diatech Pty. Ltd.
 5 <120> TITLE OF INVENTION: A method
 7 <130> FILE REFERENCE: 2404640/EJH
 9 <140> CURRENT APPLICATION NUMBER: US/09/852,058
 9 <141> CURRENT FILING DATE: 2001-08-13
 9 <150> PRIOR APPLICATION NUMBER: US 60/202,797
10 <151> PRIOR FILING DATE: 2000-05-09
12 <160> NUMBER OF SEQ ID NOS: 26
14 <170> SOFTWARE: PatentIn version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 18
18 <212> TYPE: DNA
19 <213> ORGANISM: primer
21 <400> SEQUENCE: 1
22 cagatccctg gacaggcg                                                       18
25 <210> SEQ ID NO: 2
26 <211> LENGTH: 18
27 <212> TYPE: DNA
28 <213> ORGANISM: primer
30 <400> SEQUENCE: 2
31 cagatccctg gacaggca                                                       18
34 <210> SEQ ID NO: 3
35 <211> LENGTH: 83
36 <212> TYPE: DNA
37 <213> ORGANISM: primer
39 <400> SEQUENCE: 3
40 aggaatacag gtattttgtc cttgcgcggt gagctatatg gggactatga atttctaata        60
42 ggactacttc taatctgtaa gag                                                 83
45 <210> SEQ ID NO: 4
46 <211> LENGTH: 20
47 <212> TYPE: DNA
48 <213> ORGANISM: primer
50 <400> SEQUENCE: 4
51 aatctgtaag agcagatccc                                                     20
54 <210> SEQ ID NO: 5
55 <211> LENGTH: 29
56 <212> TYPE: DNA
57 <213> ORGANISM: primer
59 <400> SEQUENCE: 5
60 tttttttttt gtccccatat agctcaccg                                          29
63 <210> SEQ ID NO: 6
64 <211> LENGTH: 18
65 <212> TYPE: DNA
66 <213> ORGANISM: primer
68 <400> SEQUENCE: 6
69 cagatccctg gacagacg                                                      18
72 <210> SEQ ID NO: 7
```

Does Not Comply
Corrected Diskette Needed

see item 10 on Error Summary Sheet
(global error)

```
 73 <211> LENGTH: 18
 74 <212> TYPE: DNA
 75 <213> ORGANISM: primer
 77 <400> SEQUENCE: 7                                                18
 78 cagatccctg gacagaca
 81 <210> SEQ ID NO: 8
 82 <211> LENGTH: 16
 83 <212> TYPE: DNA
 84 <213> ORGANISM: primer
 86 <400> SEQUENCE: 8                                                16
 87 gatccctgga cagacg
 90 <210> SEQ ID NO: 9
 91 <211> LENGTH: 16
 92 <212> TYPE: DNA
 93 <213> ORGANISM: primer
 95 <400> SEQUENCE: 9                                                16
 96 gatccctgga cagaca
 99 <210> SEQ ID NO: 10
100 <211> LENGTH: 22
101 <212> TYPE: DNA
102 <213> ORGANISM: primer
104 <400> SEQUENCE: 10                                               22
105 tgcccagtgc ttaacaagac ca
108 <210> SEQ ID NO: 11
109 <211> LENGTH: 20
110 <212> TYPE: DNA
111 <213> ORGANISM: primer
113 <400> SEQUENCE: 11                                               20
114 tgttatcaca ctggtgctaa
117 <210> SEQ ID NO: 12
118 <211> LENGTH: 67
119 <212> TYPE: DNA
120 <213> ORGANISM: primer
122 <400> SEQUENCE: 12                                               60
123 gcaggtaaag aaggcgccgc ggtgagctat atggggacta tgaatttgct ccattaaagc
                                                                     67
125 aaattgc
128 <210> SEQ ID NO: 13
129 <211> LENGTH: 49
130 <212> TYPE: DNA
131 <213> ORGANISM: primer
133 <400> SEQUENCE: 13                                               49
134 atagcgcctt ctttacctgc gttacttcga atttgcttta atggagctg
137 <210> SEQ ID NO: 14
138 <211> LENGTH: 7
139 <212> TYPE: DNA
140 <213> ORGANISM: primer
142 <400> SEQUENCE: 14                                                7
143 aagtaac
146 <210> SEQ ID NO: 15
```

Input Set : A:\2404640.diatech.method.ST25.txt
Output Set: N:\CRF3\10102001\I852058.raw

```
147 <211> LENGTH: 49
148 <212> TYPE: DNA
149 <213> ORGANISM: primer
151 <400> SEQUENCE: 15
152 atagcacctt cttttcctgc gtttgcacga atttgtttca aaggagcgg              49
155 <210> SEQ ID NO: 16
156 <211> LENGTH: 7
157 <212> TYPE: DNA
158 <213> ORGANISM: primer
160 <400> SEQUENCE: 16
161 tgcaaac                                                            7
164 <210> SEQ ID NO: 17
165 <211> LENGTH: 20
166 <212> TYPE: DNA
167 <213> ORGANISM: primer
169 <400> SEQUENCE: 17
170 ccattaaagc aaattgcaag                                              20
173 <210> SEQ ID NO: 18
174 <211> LENGTH: 21
175 <212> TYPE: DNA
176 <213> ORGANISM: primer
178 <400> SEQUENCE: 18
179 ccattaaagc aaattgctgc a                                            21
182 <210> SEQ ID NO: 19
183 <211> LENGTH: 18
184 <212> TYPE: DNA
185 <213> ORGANISM: primer
187 <400> SEQUENCE: 19
188 cagatccctg gacaggcg                                                18
191 <210> SEQ ID NO: 20
192 <211> LENGTH: 18
193 <212> TYPE: DNA
194 <213> ORGANISM: primer
196 <400> SEQUENCE: 20
197 cagatccctg gacaggca                                                18
200 <210> SEQ ID NO: 21
201 <211> LENGTH: 25
202 <212> TYPE: DNA
203 <213> ORGANISM: primer
205 <400> SEQUENCE: 21
206 tgtagagcat tacgctgcga tggat                                        25
209 <210> SEQ ID NO: 22
210 <211> LENGTH: 20
211 <212> TYPE: DNA
212 <213> ORGANISM: primer
214 <400> SEQUENCE: 22
215 tgatgctcca taacttcctg                                              20
218 <210> SEQ ID NO: 23
219 <211> LENGTH: 13
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/852,058

DATE: 10/10/2001
TIME: 17:07:04

Input Set : A:\2404640.diatech.method.ST25.txt
Output Set: N:\CRF3\10102001\I852058.raw

```
220 <212> TYPE: DNA
221 <213> ORGANISM: primer
223 <400> SEQUENCE: 23
                                                        13
224 ctgtggaatt gag
227 <210> SEQ ID NO: 24
228 <211> LENGTH: 13
229 <212> TYPE: DNA
230 <213> ORGANISM: primer
232 <400> SEQUENCE: 24
                                                        13
233 ctgtggaatt gag
236 <210> SEQ ID NO: 25
237 <211> LENGTH: 13
238 <212> TYPE: DNA
239 <213> ORGANISM: primer
241 <400> SEQUENCE: 25
                                                        13
242 ctctggaatt gat
245 <210> SEQ ID NO: 26
246 <211> LENGTH: 30
247 <212> TYPE: DNA
248 <213> ORGANISM: primer
250 <400> SEQUENCE: 26
                                                        30
251 atcgcgaaaa ctgtggaatt gatcagcgtt
```

10/10/01

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/852,058

DATE: 10/10/2001
TIME: 17:07:05

Input Set : A:\2404640.diatech.method.ST25.txt
Output Set: N:\CRF3\10102001\I852058.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date